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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/647,067	09/25/2000	Aaron J. W. Hsueh	EL539 356 27	3881

24353 7590 11/06/2002

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EXAMINER
BUNNER, BRIDGET E

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 11/06/2002 13

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/647,067	HSUEH ET AL.	
	Examiner	Art Unit	
	Bridget E. Bunner	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *12 August 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-18* is/are pending in the application.

4a) Of the above claim(s) *12-17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-11 and 18* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1-18* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *3, 6* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Election/Restrictions

Applicant's election of Group A, claims 1-11 and 18 in Paper No. 9 (22 April 2002) is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Additionally, Applicant's election of LGR7, SEQ ID NO: 7, in Paper No. 11 (12 August 2002) is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claims 12-17 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected group, there being no allowable generic or linking claim. Election was made **without** traverse in Paper No. 9 (22 April 2002).

Claims 1-11 and 18 are under consideration in the instant application.

Sequence Compliance

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). **Specifically, the sequences disclosed in Figures 5 and 6 are not accompanied by the required reference to the relevant sequence identifiers.** This application fails to comply with the requirements of 37 CFR 1.821 through 1.825. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825).

Specification

2. The disclosure is objected to because of the following informalities:

3. This application does not contain an abstract of the disclosure as required by 37 CFR 1.72(b). An abstract on a separate sheet is required.

4. An application in which the benefits of an earlier application are desired must contain a specific reference to the prior application(s) in the first sentence of the specification or in an application data sheet (37 CFR 1.78(a)(2) and (a)(5)).

Appropriate correction is required.

Claim Objections

5. Claims 1-7, 10-11, and 18 are objected to because of the following informalities:

5a. Claims 1-7, 10-11, and 18 recite non-elected groups (not related to LGR7).

Appropriate correction is required.

Claim Rejections - 35 USC § 101 and § 112, first paragraph

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 1-11 and 18 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a credible, specific and substantial asserted utility or a well established utility. Novel biological molecules lack well established utility and must undergo extensive experimentation.

Claims 1-11 and 18 are directed to an isolated nucleic acid encoding a mammalian protein consisting of LGR7 and wherein the protein has the amino acid sequence of SEQ ID NO: 8. The claims also recite an isolated nucleic acid wherein the nucleotide sequence has the sequence consisting of SEQ ID NO: 7. The claims recite that an isolated nucleic acid comprising at least 18 or 50 contiguous nucleotides of SEQ ID NO: 7. The claims recite an expression cassette, a host cell, and a method of producing a mammalian protein. The claims are also directed to a purified polypeptide composition comprising at least 50 weight % of the protein present as a mammalian protein consisting of LGR7, or a fragment thereof. The claims are directed to a method of screening a sample for the presence of a ligand for a LGR7 receptor.

The specification asserts that the human LGR7 nucleic acid (SEQ ID NO: 7) and polypeptide (SEQ ID NO: 8) of the present invention are novel mammalian receptors of the G-protein coupled, seven transmembrane family of proteins, specifically the subfamily which is characterized by the presence of extracellular leucine rich repeat regions. However, the instant specification does not teach any significance or functional characteristics of the human LGR7 nucleic acid (SEQ ID NO: 7) or polypeptide (SEQ ID NO: 8). The specification also does not disclose any methods or working examples that indicate the nucleic acid and polypeptide of the instant invention are involved in any cellular activities. Since significant further research would be required of the skilled artisan to determine how the claimed polypeptide is involved in a any

activity, the asserted utilities are not substantial. The specification asserts the following as patentable utilities for the claimed putative LGR7 nucleic acid and polypeptide (SEQ ID NO: 7 and SEQ ID NO: 8, respectively):

1) to identify homologous or related genes (pg 2, line 11; pg 3, line 6; pg 4-5)

2) for the production of compositions that modulate the expression or function of the subject protein (pg 2, lines 11-12; pg 3, lines 6-7)

3) to identify endogenous ligands for the receptor (pg 2, lines 12-13; pg 3, lines 6-7; pg 20)

4) to generate functional binding proteins for the neutralization of the actions of endogenous ligands (pg 2, lines 13-14; pg 20)

5) in gene or protein therapy (pg 2, lines 14-15; pg 3, line 8; pg 15)

6) to map functional regions of the protein (pg 2, line 15; pg 3, line 9)

7) to produce antibodies (pg 3, lines 10-11; pg 11)

8) to diagnose a disease state or a genetic predisposition to a disease state (pg 12-14)

9) to generate transgenic, non-human animals or cell lines (pg 17, lines 27-32 through pg 19)

Each of these shall be addressed in turn.

1) to identify homologous or related genes. This asserted utility is credible but not substantial or specific. Such assays can be performed with any nucleic acid or polypeptide. Further, the specification does not disclose specific DNA or protein sequences for use as probes to identify the related gene or protein. Further, the specification discloses nothing specific or substantial about the homologous gene or protein that is identified by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

2) for the production of compositions that modulate the expression or function of the subject protein. This asserted utility is credible but not specific or substantial. Compositions can be produced to modulate the function and expression of any protein. The specification discloses nothing specific or substantial about the compositions that can be produced by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

3) to identify endogenous ligands for the receptor. This asserted utility is credible but not substantial or specific. Such assays can be performed with any polypeptide. Further, the specification discloses nothing specific or substantial about the endogenous ligands that are identified by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

4) to generate functional binding proteins for the neutralization of the actions of endogenous ligands. This asserted utility is credible but not specific or substantial. Such assays can be performed with any polypeptide. Additionally, the specification discloses nothing specific or substantial for the binding proteins that can be generated by this method. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

5) in gene or protein therapy. This asserted utility is credible but not specific or substantial. Such can be performed for any nucleic acid or polypeptide. Further, the specification does not disclose diseases associated with a mutated, deleted, or translocated LGR7 gene or protein (SEQ ID NOs: 7 and 8, respectively). Significant further experimentation would be required of the skilled artisan to identify individuals with such a disease and to determine the

route of administration of the gene or protein, as well as quantity and duration of treatment. Since this asserted utility is also not presented in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

6) to map functional regions of the protein. This asserted utility is credible but not substantial or specific. Such assays can be performed with any protein. Further, the specification does not disclose any specific regions of the protein that would be targeted. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

7) to produce antibodies. This asserted utility is credible but not substantial or specific. Antibodies can be made to any polypeptide. However, if the specification discloses nothing specific and substantial about the polypeptide, therefore both polypeptide and its antibodies have no patentable utility. Since this asserted utility is also not presented in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

8) to diagnose a disease state or a genetic predisposition to a disease state. This asserted utility is credible but not specific or substantial. The specification does not disclose disorders associated with a mutated, deleted, or translocated LGR7 gene (SEQ ID NO: 7). Significant further experimentation would be required of the skilled artisan to identify individuals with such a disease. Since this asserted utility is also not presented in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

9) to generate transgenic, non-human animals or cell lines. This asserted utility is credible but not specific or substantial. The specification does not disclose diseases associated with a mutated, deleted, or translocated LGR7 gene (SEQ ID NO: 7). Significant further

experimentation would be required of the skilled artisan to identify such a disease. The specification discloses nothing about whether the gene will be "knocked in" or "knocked out" or what specific tissues and cells are being targeted. Since this asserted utility is also not present in mature form, so that it could be readily used in a real world sense, the asserted utility is not substantial.

7. Claims 1-11 and 18 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

(7a.) Furthermore, claims 5-6 and 11 recite an isolated nucleic acid comprising at least 18 or 50 contiguous nucleotides of the sequence consisting of SEQ ID NO: 7. The claims also recite a purified polypeptide composition comprising at least 50 weight % of the protein present as a mammalian protein consisting of LGR7, or a fragment thereof.

The specification teaches that the sequence of the LGR7 gene "may be mutated in various ways known in the art to generate targeted changes in promoter strength, sequence of the encoded protein, etc. (pg 8, lines 11-13). The specification also discloses that the sequence changes may be substitutions, insertions, deletions, or a combination thereof (pg 8, lines 17-18). However, the specification also does not teach LGR7 nucleic acid variants or polypeptide variants. Further, the specification does not teach any functional or structural characteristics of the variants or fragments of the nucleic acid of SEQ ID NO: 7 or the polypeptide of SEQ ID NO: 8.

The problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These regions can tolerate only relatively conservative substitutions or no substitutions (see Wells, 1990, Biochemistry 29:8509-8517; Ngo et al., 1994, The Protein Folding Problem and Tertiary Structure Prediction, pp. 492-495). However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to use the current invention as a starting point for further experimentation. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often

destroy activity. The art recognizes that function cannot be predicted from structure alone (Bork, 2000, Genome Research 10:398-400; Skolnick et al., 2000, Trends in Biotech. 18(1):34-39, especially p. 36 at Box 2; Doerks et al., 1998, Trends in Genetics 14:248-250; Smith et al., 1997, Nature Biotechnology 15:1222-1223; Brenner, 1999, Trends in Genetics 15:132-133; Bork et al., 1996, Trends in Genetics 12:425-427).

Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations and also embrace a broad class of structural fragments and variants, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

(7b). Additionally, claim 18 is rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Claim 18 recites a method of screening a sample for the presence of a ligand for a receptor comprising contacting said sample with a LGR7 receptor or a mimetic thereof, and detecting the presence of a binding event between said receptor and ligand in said sample.

The specification teaches that the nucleic acids and polypeptide compositions of the instant application can be utilized to identify endogenous ligands for the LGR7 orphan receptor. However, the specification does not teach any methods or working examples that identify ligands that bind to human LGR7 receptor of SEQ ID NO: 8. The specification does not disclose contacting any sample with a LGR7 receptor and detecting a binding event between the receptor and any ligand. The specification of the instant application does not disclose the identity of any ligand capable of binding the LGR7 receptor via the claimed method. There is no guidance in the specification as to any specific procedure for screening a sample for a ligand that binds the LGR7 receptor. Since there is inadequate guidance in the specification, the skilled artisan must use the current invention as a starting point for further experimentation. Such trial and error experimentation is considered undue. Furthermore, since the specification provides little guidance regarding what sort of samples or ligands should be screened for binding the LGR7 receptor, the skilled artisan must resort to trial and error experimentation to determine which samples or ligands might yield one with the desired activity. Such trial and error experimentation is considered undue.

Due to the large quantity of experimentation necessary to identify any ligand capable of binding the LGR7 receptor, the lack of direction/guidance presented in the specification regarding the same, the absence of working examples directed to the same, the complex nature of the invention, and the breadth of the claims which fail to recite any compound limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

8. Claims 5-6 and 11 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 5-6 and 11 recite an isolated nucleic acid comprising at least 18 or 50 contiguous nucleotides of the sequence consisting of SEQ ID NO: 7. The claims also recite a purified polypeptide composition comprising at least 50 weight % of the protein present as a mammalian protein consisting of LGR7, or a fragment thereof.

The specification teaches that the sequence of the LGR7 gene "may be mutated in various ways known in the art to generate targeted changes in promoter strength, sequence of the encoded protein, etc. (pg 8, lines 11-13). The specification also discloses that the sequence changes may be substitutions, insertions, deletions, or a combination thereof (pg 8, lines 17-18). However, the specification does not teach functional or structural characteristics of the nucleic acid and polypeptide in the context of a cell or organism. The description of one LGR7 nucleic acid species (SEQ ID NO: 7) and one LGR7 polypeptide species (SEQ ID NO: 8) is not adequate written description of an entire genus of functionally equivalent polynucleotides and polypeptides which incorporate all variants and fragments with at least 18 or 50 contiguous nucleotides of the sequence consisting of SEQ ID NO: 7 or all fragments of protein consisting of the amino acid sequence of SEQ ID NO: 8.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry,

whatever is now claimed" (See page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed" (See *Vas-Cath* at page 1116).

With the exception of the sequences referred to above, the skilled artisan cannot envision the detailed chemical structure of the encompassed nucleic acids, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only an isolated nucleic acid comprising the nucleotide sequence consisting of SEQ ID NO: 7 and a purified polypeptide composition comprising at least 50 weight % of the protein present as a mammalian protein consisting of LGR7, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

9. Claims 1-11 and 18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

10. Regarding claims 1-11 and 18, the acronyms "LGR7", "LGR4", and "LGR5" render the claims vague and indefinite. Abbreviations should be spelled out in all independent claims for clarity.

11. Regarding claims 4-7, the phrase "complementary sequence thereof" renders the claims indefinite because it is unclear whether "complementary sequence thereof" refers to the entire nucleic acid sequence complement or variants and fragments of the complement.

12. The term "substantially identical" in claim 3 is a relative term which renders the claim indefinite. The term "substantially identical" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. It cannot be determined if "substantially identical" means that the amino acid sequence is 10%, 25%, 50%, 100%, etc. identical to the amino acid sequence of SEQ ID NO: 8.

13. Stringency is relative, and the art does not recognize a single set of conditions as stringent. The specification also does not provide an unambiguous definition for the term. In the absence of a recitation of clear hybridization conditions (e.g., "hybridizes at wash conditions of **A** X SSC and **B** % SDS at **C**°C"), claim 7 fails to define the metes and bounds of the varying structures of polynucleotides recited in the claimed methods.

14. The term "50 weight %" in claim 11 is a relative term which renders the claim indefinite. The term "50 weight %" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. It cannot be determined if the claim is referring to the molecular weight of the protein. If so, the claim must include the method by which the molecular weight is calculated that determines the numerical value of LGR7.

15. The term "binding event" in claim 18 is a relative term which renders the claim indefinite. The term "binding event" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. It cannot be determined if "binding event" simply means detecting the binding between the receptor or ligand or if it means detecting fluorescence, detecting color change of the media, measuring cell growth, etc.

16. The term "mimetic" in claim 18 is a relative term which renders the claim indefinite. The term "mimetic" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. It cannot be determined if "mimetic" means an organic compound, an inorganic compound, a polypeptide 50% identical to the LGR7 receptor, etc.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

17. Claims 5-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Hillier et al. (Accession No. AA122079; EST database; 19 November 1996).

Hillier et al. teaches an isolated nucleic acid comprising at least 18 and 50 contiguous nucleotides of the sequence consisting of SEQ ID NO: 7. (See sequence alignment attached to this Office Action as Appendix A; see nucleotides 3218-3424 of SEQ ID NO: 7 of the instant application and nucleotides 386-180 of Hillier et al.)

Conclusion

No claims are allowable.

The art made of record and not relied upon is considered pertinent to applicant's disclosure:

Hsu et al. Molec Endocrin 14 : 1257-1271, 2000.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Bridget E. Bunner whose telephone number is (703) 305-7148. The examiner can normally be reached on 8:30-5:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Kunz can be reached on (703) 308-4623. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 872-9306 for regular communications and (703) 872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 872-9305.

BEB
Art Unit 1647
October 25, 2002

Elyabeth C. Kemmerer

ELIZABETH KEMMERER
PRIMARY EXAMINER

Appendix A

RESULT 5
AA122079/c
LOCUS AA122079 454 bp mRNA linear EST 19-NOV-1996
DEFINITION zk93g10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490434 3', mRNA sequence.
ACCESSION AA122079
VERSION AA122079.1 GI:1678117
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 454)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 345.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:490434"
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/sex="female"
/dev_stage="adult"
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/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

BASE COUNT 150 a 76 c 70 g 142 t 16 others
ORIGIN

Query Match 11.3%; Score 405; DB 9; Length 454;
Best Local Similarity 95.1%; Pred. No. 2.6e-69;
Matches 409; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy   3151 tgttttaagaacagacctaagtggtttaattcacccactttagatgggtgaatgttatgg 3210
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Db    453 TGTTTTAAGAACAGACCTAAGTGGTTTAATTCACCCACTTTAGATGGGTGAATGTTATGG 394

Qy   3211 tgtgtgaaatatctcagtaaagcagttaaaaggaaaaagagctggaatgcactgattcag 3270
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Db    393 TGTGTGNAATATCTCAGTAAAGCAGTTAAAAGGAAAAAGAGCTGGAATGCACTGATTCAG 334

Qy   3271 gaacttaatttcaggaaggaaaggtctgtatgtacacatttcactttaagcagaaaatct 3330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 GAACTTAATTTCAGGAAGGAAAGGTCTGTATGTACACATTTCACTTTAAGCAGAAAATCT 274

Qy   3331 ttcttcaagaaatgactttacttttctctttgcactgccagcacgtgagatactaacttttt 3390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 TTCTTCAAGAAATGACTTTACTTTCTCTTTGCACTGCCAGCACGTGAGATACTAACTTTT 214

Qy   3391 taactagttgttcttctctagtctctacgttattagnatttttgctttcataatgtgaa 3450
          |||||||||||||||||||||||||||||||||| | ||||| |||| |||||||||| |
Db    213 TAACTAGTTGTTCTTCTCTAGTCTCTACGTTATTNGAATTTTNTGCTNTCATAATGTGNA 154

Qy   3451 acctttaagcaggagaagaaaatgttttcagatagtttcaaatacnccaaaaatgtttgc 3510
          |||||||||||||||||| | ||||| |||| |||||||| |||||||| ||||||||||
Db    153 ACCTTTAAGCAGGAGAAGCANATGTTNTCAGNTAGTTTCANATACNCCNAAAATGTTTGA 94

Qy   3511 aacacaaaaatactggaatcnaaccataatgcccttattgaatatatagttgtatagntt 3570
          ||||||| |||||||||||| |||||||||| |||||||||| | ||||| ||| ||
Db     93 AACACAANAATACTGGAATCAAACCATAATGCACTTATTGAATATCTNGTTGTNTAGATT 34

Qy   3571 tgttctgaaa 3580
          ||||||||| |
Db     33 TGTTCTGACA 24
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